

GenCode version 5.1.3
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OM protein - protein search, using sw mod-1

Run on: January 16, 2003 16:42:17, Search time 2 21:29 Seconds
(without alignments)
58,517 Million cell updates/sec

Title: US-09-856-070-25

Perfect score: 23

Sequence: 1 MLRLQ 5

Scoring table: BLOSUM62

Gapop 10 0 Gapext 0.5

Searched: 283224 seqs, 9613422 residues 283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	23	100.0	120	2	F72450	hypothetical prote
2	23	100.0	157	2	H69461	conserved hypothe
3	23	100.0	160	2	A71360	conserved hypothe
4	23	100.0	196	1	R6PT19	ribosomal protein
5	23	100.0	196	2	A36554	ribosomal protein
6	23	100.0	196	2	A48992	ribosomal protein
7	23	100.0	220	2	A71561	ABC transporter, A
8	23	100.0	220	2	A61204	ABC transporter, A
9	23	100.0	244	2	S36703	gene 8 protein - e
10	23	100.0	245	1	W8HEA7	gene 8 protein - e
11	23	100.0	272	2	A81553	B. subtilis Yj88 p
12	23	100.0	272	2	A81195	B. subtilis Yj88 p
13	23	100.0	288	2	T41101	Cylin-dependent c
14	23	100.0	313	2	A82737	aspartate carboxyl
15	23	100.0	322	2	H65583	aspartate carboxyl
16	23	100.0	322	2	A83593	aspartate carboxyl
17	23	100.0	326	2	S36335	U2 snRNP 40K prote
18	23	100.0	328	2	D83655	DNA polymerase III
19	23	100.0	332	2	B87552	aspartate carboxyl
20	23	100.0	334	2	A56144	aspartate carboxyl
21	23	100.0	334	2	H83545	aspartate carboxyl
22	23	100.0	355	2	F96820	Probable form ABC
23	23	100.0	361	2	B97518	(AY037523) aspart
24	23	100.0	390	2	S56560	hypothetical, 43.6K
25	23	100.0	390	2	p91261	hypothetical prote
26	23	100.0	390	2	S96132	hypothetical prote
27	23	100.0	440	2	B54410	hypothetical prote
28	23	100.0	453	2	T42428	mitochondrial proc
29	23	100.0	454	2	S61455	flagellar hook pro

30	23	100.0	457	2	T50402	probable mitochond
31	23	100.0	505	2	T64189	amidophosphoribos
32	23	100.0	505	2	A50348	amidophosphoribos
33	23	100.0	581	2	T45886	ezrin - bovine
34	23	100.0	586	1	A34460	ezrin [validated]
35	23	100.0	586	1	B41129	ezrin - mouse
36	23	100.0	610	2	T19333	hypothetical prote
37	23	100.0	630	2	T47177	glucan 1,4-alpha-g
38	23	100.0	748	2	T49633	hypothetical prote
39	23	100.0	785	2	B85036	hypothetical prote
40	23	100.0	606	2	T60476	probable disease r
41	23	100.0	1428	2	T39476	probable ATP depen
42	23	100.0	1690	2	T13030	microtubule bindin
43	21	91.3	100	2	A81097	primesomal replica
44	21	91.3	100	2	G81845	primesomal replica
45	21	91.3	109	2	H95038	hypothetical prote

ALIGNMENTS

RESULT 1
F72450
Hypothetical Protein AFH2250 Aeropyrum pernix (Strain KI)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #seqs_in_revision: 90-Aug-1999 #text_change: 05-Jun-2000
C:Accession: F72450
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jinnou, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6: 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyperthermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:95310339; PMID:10482966
A:Accession: F72450
A>Status: preliminary
A:Molecule type: DNA
A:Accession: F72450
A:Accession: F72450
A:Experimental source: strain KI
C:Genetics:
A:Gene: APE2250
C:Superfamily: Aeropyrum pernix hypothetical protein APE2250

Query Match 100.0% Score 23; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
|||||
DB 1 MLRLQ 5

RESULT 2
H69461
Conserved hypothetical protein AF1697 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #seqs_in_revision: 05-Dec-1997 #text_change: 05-Oct-1999
C:Accession: H69461
R:Klenk, H.P.; Graydon, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
g, F.; Schmidt, K.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Chick, A.; Zhou, L.; Overback, R.; Gonyea, J.D.; Weidman, J.E.; McDonald, L.
Nature 390: 364-370, 1997
A:Authors: Overback, L.; Gordon, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Reese, C.K.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A65250; MUID:98649343; PMID:9383475
A:Accession: H69461
A>Status: preliminary
A:Molecule type: DNA
A:Accession: F72450
A:Accession: F72450
A:Experimental source: strain KI
C:Genetics:
A:Gene: APE2250
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M01553

Query Match 100.0% Score 23; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
|||||
DB 1 MLRLQ 5

A:Cross-references: GDB:128847; OMIM:180466
 A:Map position: 17q11-17q11
 C:Superfamily: rat ribosomal protein L19
 C:Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 23; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 I I I I I
 DB 3 MLRLQ 7

RESULT 7

AF1561
 ABC transporter, ATP-binding protein homolog lin1031 [imported] - *Listeria innocua* (strain ABC)
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AF1561
 R:Glaser, P., Frangeul, L., Buchrieser, C., Amend, A., Rapoport, F., Berche, F., Blauwkamp, J., Dominguez-Bernal, G., Duchaud, E., Durand, L., Dussurget, O., Entian, K., Fsihi, H., Jones, L.M., Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J., Kuhn, M., Kunst, F., Kurapkak, G., Madueno, E., Maitouram, A., Maitouram, E., Schlueter, T., Simoes, N., Tieszen, A., Vazquez-Boland, J.A., Voss, H., Weiland, O.F.
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AF1561; MIM:2153279; EMBL:1167966
 A:Accession: AF1561
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 (GLA)
 A:Cross-references: AF1561; EMBL:1167966; EMBL:1167966; EMBL:1167966; EMBL:1167966; EMBL:1167966
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lin1031

Query Match 100.0%; Score 23; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 I I I I I
 DB 1 MLRLQ 5

RESULT 8

AG1204
 ABC transporter, ATP-binding protein homolog lin1031 [imported] - *Listeria monocytogenes*
 C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1204
 R:Glaser, P., Frangeul, L., Buchrieser, C., Amend, A., Rapoport, F., Berche, F., Blauwkamp, J., Dominguez-Bernal, G., Duchaud, E., Durand, L., Dussurget, O., Entian, K., Fsihi, H., Jones, L.M., Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J., Kuhn, M., Kunst, F., Kurapkak, G., Madueno, E., Maitouram, A., Maitouram, E., Schlueter, T., Simoes, N., Tieszen, A., Vazquez-Boland, J.A., Voss, H., Weiland, O.F.
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AG1204; MIM:2153279; EMBL:1167966
 A:Accession: AG1204
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 (GLA)
 A:Cross-references: GDB:128847; OMIM:180466
 A:Experimental source: strain EGB-e
 C:Genetics:
 A:Gene: lin1031

Query Match 100.0%; Score 23; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 I I I I I
 DB 1 MLRLQ 5

RESULT 9

S36703
 gene 8 protein - equine herpesvirus 4
 N:Alternate names: B2 protein
 C:Species: equine herpesvirus 4
 C:Date: 04-Jan-1994 #sequence_revision 12-May-1995 #text_change 12-May-1995
 C:Accession: S36703; F42551
 R:Riggio, P.
 submitted to the EMBL Data Library, November 1989
 A:Reference number: S36703
 A:Accession: S36703
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-241 (GLA)
 A:Cross-references: EMBL:X17684; NID:q332459; PDB:0AA35668.1; PDB:0459216
 R:Telford, E.A., Watson, M.S., Perry, J., Cullis, A.A., Davison, A.J.
 J. Gen. Virol. 79, 1197-1203, 1998
 A:Title: The DNA sequence of equine herpesvirus-4.
 A:Reference number: S36703; F42551
 A:Accession: F42551
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-244 (GLA)
 A:Cross-references: EMBL:AF63667; NID:q332459; PDB:0AA35668.1; PDB:0459216
 A:Experimental source: strain NS80567
 C:Genetics:
 A:Gene: 8
 C:Superfamily: varicella-zoster virus gene 7 protein

Query Match 100.0%; Score 23; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 I I I I I
 DB 34 MLRLQ 38

RESULT 10

WZBEA7
 gene 8 protein - equine herpesvirus 1 (strain AB4p)
 C:Species: equine herpesvirus 1
 A:Note: host Equus caballus (domestic horse)
 C:Date: 10-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
 C:Accession: F36795
 R:Telford, E.A., Watson, M.S., McBride, K., Davison, A.J.
 submitted to GenBank, March 1992
 A:Description: The DNA sequence of equine herpesvirus-1.
 A:Reference number: A36805
 A:Accession: F36795
 A:Molecule type: DNA
 A:Residues: 1-245 (GLA)
 A:Cross-references: GB:M86664; NID:q330791; PDB:0AA02443.1; PDB:q330800
 R:Telford, E.A., Watson, M.S., McBride, K., Davison, A.J.
 Virology 189, 304-316, 1992
 A:Title: The DNA sequence of equine herpesvirus-1.
 A:Reference number: A41831; MIM:229556; PDB:0418606
 A:Contents: annotation; possible protein-coding frames
 A:Note: neither amino acid nor nucleotide sequence is given
 C:Genetics:
 A:Gene: 8
 C:Superfamily: varicella-zoster virus gene 7 protein

Query Match 100.0%; Score 23; DB 1; Length 245;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5

db 33 MLRLO 37
|||||

RESULT 11

AB1553
B. subtilis Yjbl protein homolog lin0963 [imported] - Listeria innocua (strain Clip11262)
C:Date: 27-Nov-2001 #sequence_revision 27 Nov 2001 #text_change 27 Nov-2001
C:Accession: AB1553
R:Glaser, P.; Franquet, L.; Huehrli, C.; Amend, A.; Baguer, F.; Berche, P.; Bieckel, D.; Dominguez-Bernal, G.; Durand, E.; Durand, L.; Dussurget, G.; Entian, K.D.; Fsihl, H.; Science 294, 849-852, 2001
A:Authors: Kieft, J.; Kuhn, M.; Kunst, F.; Kurokawa, G.; Madueno, F.; Maitournam, A.; Maitournam, F.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AB1553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <GLA>
A:Cross-references: GB:AL592022; PDB:CAQ96194.1; PID:q16413422; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0963

Query Match 100.0% Score 23; DB 2; Length 272;
Best Local Similarity 100.0% Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLO 5
|||||

DB 37 MLRLO 41

RESULT 12

AB1195
B. subtilis Yjbl protein homolog lin0964 [imported] - Listeria monocytogenes (strain B0)
C:Species: Listeria monocytogenes
C:Date: 27 Nov 2001 #sequence_revision 27 Nov 2001 #text_change 27 Nov 2001
C:Accession: AB1195
R:Glaser, P.; Franquet, L.; Huehrli, C.; Amend, A.; Baguer, F.; Berche, P.; Bieckel, D.; Dominguez-Bernal, G.; Durand, E.; Durand, L.; Dussurget, G.; Entian, K.D.; Fsihl, H.; Science 294, 849-852, 2001
A:Authors: Kieft, J.; Kuhn, M.; Kunst, F.; Kurokawa, G.; Madueno, F.; Maitournam, A.; Maitournam, F.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AB1195
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <GLA>
A:Cross-references: GB:AL592022; PDB:CAQ96194.1; PID:q16410366; GSPDB:GN00177
A:Experimental source: strain B0
C:Genetics:
A:Gene: lin0964

Query Match 100.0% Score 23; DB 2; Length 272;
Best Local Similarity 100.0% Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLO 5
|||||

DB 37 MLRLO 41

RESULT 13

AB1101
cyclic dependent edc2 cdc28 family serine/threonine protein kinase fission yeast (Sch)
C:Species: Schizosaccharomyces pombe
C:Date: 03 Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000

C:Accession: T41101
R:Purnelle, B.; Golliau, A.; Wood, V.; Rajandream, M.A.; Bartell, B.G.; submitted to the EMBL Data Library, September 1998
A:Reference number: Z21964
A:Accession: T41101
A:Status: preliminary; translated from GE/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-388 <PDB>
A:Cross-references: EMBL:AL031535; PDB:CAA20759.1; GSPDB:GN00068; SDB:SDC1604.11
A:Experimental source: strain 972h; cosmid c1604
C:Genetics:
A:Gene: SPDB:SPC16C4.11
A:Map position: 3
A:Indels: 10/1
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 100.0% Score 23; DB 2; Length 288;
Best Local Similarity 100.0% Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLO 5
|||||

DB 265 MLRLO 269

RESULT 14

AD2737
aspartate carbamoyl transferase [imported] Agrobacterium tumefaciens (strain C58, D)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01 Feb-2002
C:Accession: AD2737
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woeherage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClard, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <KIP>
A:Cross-references: GB:AB008688; PDB:1AAL42414.1; PID:q1773916; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: pyrB
A:Map position: circular chromosome
C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase

Query Match 100.0% Score 23; DB 2; Length 313;
Best Local Similarity 100.0% Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLO 5
|||||

DB 222 MLRLO 226

RESULT 15

HA2583
aspartate carbamoyltransferase XF2226 [imported] Xylella fastidiosa (strain 9650)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02 Sep 2000
C:Accession: HA2583
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: HA2583; PMID:1091047
A:Note: for a complete list of authors see reference number A59428 below
A:Accession: HA2583
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-322 <SIM>
A:Cross-references: GB:AF004035; GB:AF003849; NID:g9107371; PIDD:AAF85025.1; GSPDR:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reimach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; N
Briones, M.P.S.; Bueno, M.P.P.; Canarqo, A.A.; Canarqo, I.E.A.; Carraro, D.M.; Carre, H
as Neto, R.; Bocana, C.; Elidorty, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laip
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, F.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.C.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J.; de M., de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2226
C:Superfamily: ornithine carbamoyltransferase, aspartate/ornithine carbamoyltransferase

Query Match 100.0%; Score 23; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. NO. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRQ 5
DB 237 MLRQ 241

Search completed: January 16, 2003, 16:57:53
Job time : 9.21429 secs

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

2. The second part of the document is a list of the topics that were discussed at the meeting. The topics are listed in alphabetical order.

3. The third part of the document is a list of the actions that were taken at the meeting. The actions are listed in alphabetical order.

4. The fourth part of the document is a list of the resolutions that were adopted at the meeting. The resolutions are listed in alphabetical order.

5. The fifth part of the document is a list of the recommendations that were made at the meeting. The recommendations are listed in alphabetical order.